

1/4

1	TCCCATACAGGCCCCACCATGAAGGGTTTCACAGCCACTCTCTTCTCTGGACTCTGAT	60
1	MetLysGlyPheThrAlaThrLeuPheLeuTrpThrLeuI	14
	M K G F T A T L F L W T L I	
61	TTTTCCAGCTGCAGTGGAGGCGGCGGTGGGAAAGCCTGGCCACACACGTGGTCTGTAG	120
15	ePheProSerCysSerGlyGlyGlyGlyGlyLysAlaTrpProThrHisValValCysSe	34
	F P S C S G G G G G K A W P T H V V C S	
121	CGACAGCGGCTTGAAGTGCTCTACCAGAGTTGCGATCCATTACAAGATTTGGCTTTTC	180
35	rAspSerGlyLeuGluValLeuTyrGlnSerCysAspProLeuGlnAspPheGlyPheSe	54
	D S G L E V L Y Q S C D P L Q D F G F S	
181	TGTTGAAAAGTGTTCGAAGCAATTAATAATCAAATATCAACATTAGATTTGGAATTATTCT	240
55	rValGluLysCysSerLysGlnLeuLysSerAsnIleAsnIleArgPheGlyIleIleLe	74
	V E K C S K Q L K S N I N I R F G I I L	
241	GAGAGAGGACATCAAAGAGCTTTTTCTTGACCTAGCTCTCATGTCTCAAGGCTCATCTGT	300
75	uArgGluAspIleLysGluLeuPheLeuAspLeuAlaLeuMetSerGlnGlySerSerVa	94
	R E D I K E L F L D L A L M S Q G S S V	
301	TTTGAATTTCTCCTATCCCATCTGTGAGGCGGCTCTGCCAAGTTTTCTTTCTGTGGAAG	360
95	lLeuAsnPheSerTyrProIleCysGluAlaAlaLeuProLysPheSerPheCysGlyAr	114
	L N F S Y P I C E A A L P K F S F C G R	
361	AAGGAAAGGAGAGCAGATTTACTATGCTGGGCTGTCAATAATCCTGAATTTACTATTCC	420
115	gArgLysGlyGluGlnIleTyrTyrAlaGlyProValAsnAsnProGluPheThrIlePr	134
	R K G E Q I Y Y A G P V N N P E F T I P	
421	TCAGGGAGAATACCAGTTTTGCTGGAACGTACACTGAAAAACGGTCCACCGTGGCCTG	480
135	oGlnGlyGluTyrGlnValLeuLeuGluLeuTyrThrGluLysArgSerThrValAlaCy	154
	Q G E Y Q V L L E L Y T E K R S T V A C	
481	TGCCAATGCTACTATCATGTGCTCCTGACTGTGGCCTGTAGCAAAAATCAGCCAGCTG	540
155	sAlaAsnAlaThrIleMetCysSerEnd	162
	A N A T I M C S *	
541	CATCTCGTGGGACCTCCAAGCTCCTCTGACTGAACCTACTGTGGGAGGAGAAGCAGCTGA	600

FIG. 1A

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601  TGACAGAGAGAGGCTCTACAAAGAAGCGCCCCAAAGAGTGCAGCTGCTAATTTTAGTCC 660
      -----+-----+-----+-----+-----+-----+-----+
661  CAGGACCAGACATCCCCAGACTCCACAGATGTAATGAAGTCCCCGAATGTATCTGTTTCT 720
      -----+-----+-----+-----+-----+-----+-----+
721  AAGGAGCCTCTTGGCAGTCCTTAAGCAGTCTTGAGGGTCCATCCTTTTTCTCTAATTGGT 780
      -----+-----+-----+-----+-----+-----+-----+
781  CGCCTCCCACCAGACTCACCTGCTTTTCAACTTTTAGGAGTGCTTCCTCACAGTTACCA 840
      -----+-----+-----+-----+-----+-----+-----+
841  AGAAATAAAGAAAGCTGGCC 860
      -----+-----+-----+-----+-----+-----+-----+
```

Nucleotide sequence of Human MD-1 Homolog. Corresponding deduced amino-acid sequence shown below using standard three and one letter abbreviation.

FIG.1B

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Score = 344 (160.0 bits), Expect = 6.6e-44, P = 6.6e-44
 Identities = 60/133 (45%), Positives = 86/133 (64%)

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Query:   27 WPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQLKSNINIRFGIILREDIKELFLDLA  86
          WPTH VC +  LE+ Y+SCDP QDF FS+++CS      +IR ++LR+ IKEL+  +
Sbjct:   22 WPTH TVCKEENLEIYYKSCDPQQDFAFSIDRCS DVTTHTFDIRAAMVLRQSIKELYAKVD  81

Query:   87 LMSQGSSVLNFSYPICEAALPKFSFCGRRKGEQIYYAGPVNNPEFTIPQGEYQVLLKLYT  146
          L+  G +VL++S  +C  L K  FCG++KGE +YY GP+      IPQG+Y +  L
Sbjct:   62 LIINGKTVLSYSETLCGPGLSKLIFCGKKKGEHLYYEGPITLGIKEIPQGDYTITARLTN  141

Query:   147 EKRSTVACANATI  159
          E R+TVACA+ T+
Sbjct:   142 EDRATVACADFTV  154
  
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Sequence comparison between human MD-1 protein (upper line) and MD-1 protein from chicken (lower line).

FIG.2

1488,044,0003 EKS/PSC

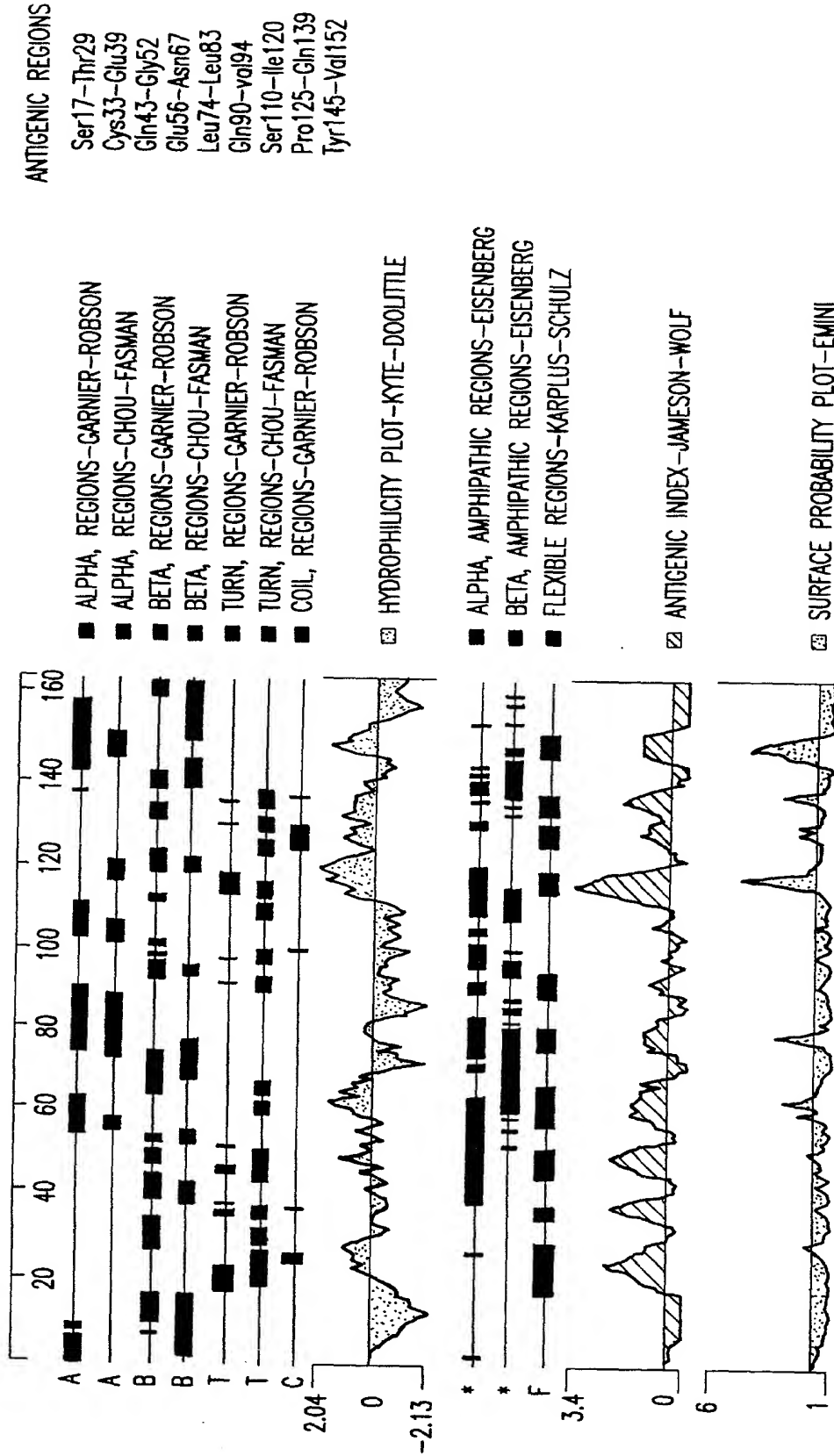


FIG.3

1	TOCCATACAGGCCCCACCATGAAGGGTTTCACAGGACACTCTCTTCTCTCTGAGCTCTGAT	60
1	MetLysGlyPheThrAlaThrLeuPheLeuTrpThrLeuI	14
	M K G F T A T L F L W T L I	
61	TTTTCCAGCTGCAGTGGAGGCGGGTGGGAAAGCCTGGCCACACAGTGGTCTGTAG	120
15	PheProSerCysSerGlyGlyGlyGlyGlyLysAlaTrpProThrHisValValCysSe	34
	F P S C S G G G G G K A W P T H V V C S	
121	CGACAGCGGCTTGGAAAGTGGCTCTAACAGAGTTGGATCCATTACAAGATTGGGCTTTTC	180
35	rAspSerGlyLeuGluValLeuTyrGlnSerCysAspProLeuGlnAspPheGlyPheSe	54
	D S G L E V L Y Q S C D P L Q D F G F S	
181	TGTTGAAAAGTGTTCAGAGCAATTAAATCAATATCAACATTAGATTGGAATTATCT	240
55	rValGluLysCysSerLysGlnLeuLysSerAsnIleAsnIleArgPheGlyIleIleLe	74
	V E K C S K Q L K S N I N I R F G I I L	
241	GAGAGAGGACATCAAGAGCCTTTTTCTTGACCTAGCTCTCATGTCTCAAGGCTCATCTGT	300
75	uArgGluAspIleLysGluLeuPheLeuAspLeuAlaLeuMetSerGlnGlySerSerVa	94
	R E D I K E L F L D L A L M S Q G S S V	
301	TTTGAATTGTCTATCCCATCTGTGAGGGGGCTCTGCCCAAGTTTCTCTCTGTGGAAG	360
95	IleuAsnPheSerTyrProIleCysGluAlaAlaLeuProLysPheSerPheCysGlyAr	114
	L N F S Y P I C E A A L P K F S F C G R	
361	AAGGAAAGGAGAGCAGATTACTATGCTGGGCGCTGTCATTAATCCTGAATTACTATTC	420
115	gArgLysGlyGluGlnIleTyrTyrAlaGlyProValAsnAsnProGluPheThrIlePr	134
	R K G E Q I Y Y A G P V N N P E P T I P	
421	TCAGGGAGATAACAGGTTTTGTCTGGAAGTGTACACTGAAAAACGCTCCACCGTGGCGT	480
135	oGlnGlyGluTyrGlnValLeuLeuGluLeuTyrThrGluLysArgSerThrValAlaCy	154
	Q G E Y Q V L L E L Y T E K R S T V A C	
481	TGCCAATGCTACTATCATGTGTCTCTGACTGTGGCGCTGTAGCAAAAATCACAGCCAGCTG	540
155	sAlaAsnAlaThrIleMetCysSerEnd	162
	A N A T I M C S *	
541	CATCTGTGGGACCTCCAGGCTCTCTGACTGAACTACTGTGGGAGGAGAAGCAGCTGA	600
601	TGACACAGGAGGCTCTACAAAGAAGCGCCCCCAAGAGTGCAGCTGCTAATTTTGTGTC	660
661	CAGGACACAGACATCCCCAGACTCCACAGATGTAAATGAAGTCCCGAATGTATCTGTCTCT	720
721	AAGGAGGCTCTTGGCAGTCTTTAAGCAGTCTTGAGGGTCCCTCCCTTTTCTCTAATGGT	780
781	CGGCTCCACACAGACTCACCTGCTTTTCACTTTTTAGGAGTGCTTCTCACAGTTACCA	840
841	AGAAATAAAGAAAGCTGGCC	860

Figure 1. Nucleotide sequence of Human MD-1 Homolog. Corresponding deduced amino-acid sequence shown below using standard three and one letter abbreviation.

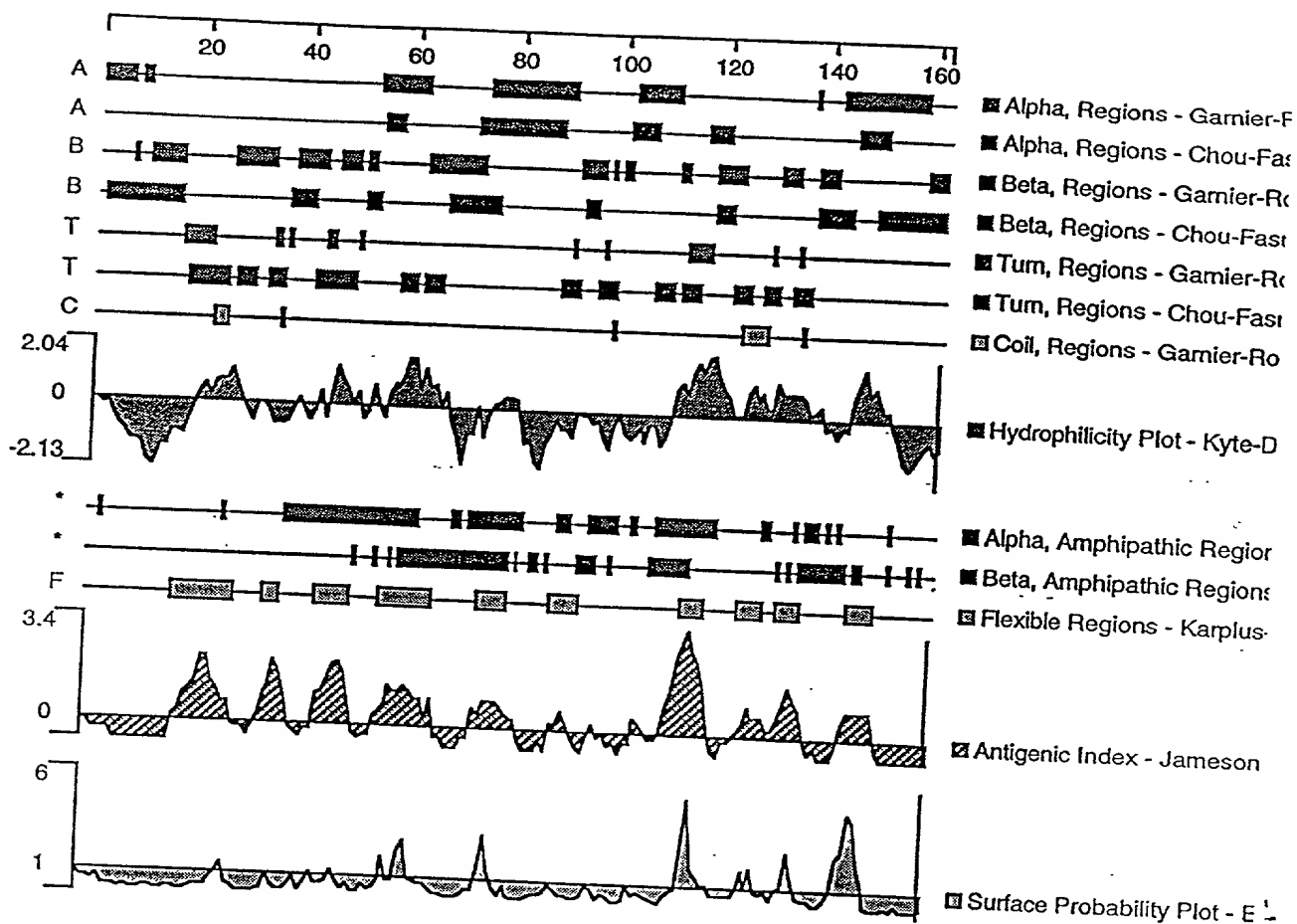


Figure 3. Analysis of the full length predicted amino acid sequence.

Antigenic regions

Ser17- Thr29
 Cys33-Glu39
 Gln43-Gly52
 Glu56-Asn67
 Leu74-Leu83
 Gln90-val94
 Ser110-Ile120
 Pro125-Gln139
 Tyr145-Val152